Annex 1: Alignment SEQ ID:29 vs Cao SEQ ID:6

```
CLUSTAL 2.0.10 multiple sequence alignment


SEQID29        MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDEDLEELEVLERKPA 60
CAOSEQID6      MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEEEDEDEDLEELEVLERKPA 60
               ************************************************************


SEQID29        AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
CAOSEQID6      AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
               ***********************************************************


SEQID29        SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
CAOSEQID6      SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
               ***********************************************************


SEQID29        SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGN 240
CAOSEQID6      SSGSVV------------------------------------------------------ 186
               ***:**


SEQID29        LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV 300
CAOSEQID6      ------------------------------------------------------------


SEQID29        IVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTKLVKEDEVVSSEKAKDSFNEKRV 360
CAOSEQID6      ------------------------------------------------------------


SEQID29        AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH 420
CAOSEQID6      ------------------------------------------------------------


SEQID29        EKDSESSNDDTSPPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDE 480
CAOSEQID6      ------------------------------------------------------------


SEQID29        KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDL 540
CAOSEQID6      ------------------------------------------------------------


SEQID29        VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI 600
CAOSEQID6      ------------------------------------------------------------


SEQID29        VMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE 660
CAOSEQID6      ------------------------------------------------------------


SEQID29        EIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELV 720
CAOSEQID6      ------------------------------------------------------------


SEQID29        EDSSPDSEPVDLFSDDSIPDVPQKQDETVMLVKESLTETSFESMIEYENKEKLSALPPEG 780
CAOSEQID6      ------------------------------------------------------------


SEQID29        GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE 840
CAOSEQID6      ------------------------------------------------------------


SEQID29        TETFSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900
CAOSEQID6      ------------------------------------------------------------


SEQID29        PHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALGHTQAEIESIVKPKVLE 960
CAOSEQID6      ------------------------------------------------------------


SEQID29        KEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF 1020
CAOSEQID6      ------------------------------VDLLYWRDIKKTGVVFGASLFLLLSLTVF 215
                                             ***************************


SEQID29        SIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 1080
CAOSEQID6      SIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 275
               ***********************************************************
```

```
SEQID29    ALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140
CAO        ALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 335
           ************************************************************

SEQID29    YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
CAO        YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373
           *************************************
```